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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/334,969DATE: 11/26/1999
TIME: 15:46:49

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This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: JAKOBSEN, Bent Karsten
2 BOUTLER, Jonathan Michael
3 <120> TITLE OF INVENTION: Multivalent T Cell Receptor Complexes
4 <130> FILE REFERENCE: 102286.410
5 <140> CURRENT APPLICATION NUMBER: US/09/334,969
6 <141> CURRENT FILING DATE: 1999-06-17
7 <150> EARLIER APPLICATION NUMBER: PCT/GB99 01583
8 <151> EARLIER FILING DATE: 1999-05-19
9 <150> EARLIER APPLICATION NUMBER: GB 9810759.2
10 <151> EARLIER FILING DATE: 1998-05-19
11 <150> EARLIER APPLICATION NUMBER: GB 9821129.5
12 <151> EARLIER FILING DATE: 1998-09-29
13 <160> NUMBER OF SEQ ID NOS: 85
14 <170> SOFTWARE: PatentIn Ver. 2.1
15 <210> SEQ ID NO 1
16 <211> LENGTH: 744
17 <212> TYPE: DNA
18 <213> ORGANISM: Artificial Sequence
19 <220> FEATURE:
20 <223> OTHER INFORMATION: Description of Artificial Sequence: Gene coding
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JM22 TCR alpha chain fused to c-jun leucine zipper
domain.
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27 gaaggctctg tcctcctggt gacagtagtt acgggtggag aagtgaagaa gctgaagaga 180
28 ctaacccttc agtttggta tgcaagaaag gacagttctc tccacatcac tgcggcccaag 240
29 cctggtgata caggcctcta cctctgtgca ggagcgggaa gccaaaggaaa tctcatctt 300
30 gaaaaaggca ctaaaactctc tttttaaacca aatatccaga accctgaccc tggccgtgtac 360
31 cagctgagag actctaaatc cagtgacaag tctgtctgcc tattcaccga ttttgattct 420
32 caaaacaaatg tggcacaaag taaggattct gatgtgtata tcacagacaa aactgtgcta 480
33 gacatgaggt ctatggactt caagagcaac agtgctgtgg cctggagcaa caaatctgac 540
34 tttgcatgtg caaacgcctt caacaacacgc attattccag aagacacaccc tttcccccagc 600
35 ccagaaagtt ccccccgggg tagaatcgcc cggctggagg aaaaagtcaa aaccttgaaa 660
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37 aaacagaaaag tcatgaacta ctag 744
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41 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: Description of Artificial Sequence: Amino acid
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 96 ttcccaccccg aggtcgctgt gtttgaacca tcagaagcag agatctccca cacccaaag 420
 97 gcccacactgg tggcctggc cacaggcttc taccggcacc acgtggagct gagctgggtgg 480
 98 gtgaatggga aggaggtgca cagtgggtc agcacagacc cgccggccct caaggagcag 540
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 101 gacgagtgga cccaggatag ggccaaacct gtcacccaga tcgtcagcgc cgaggcctgg 720
 102 ggttagagcag accccggggg tctgactgat acactccaag cggagacaga tcaacttcaa 780
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108 <213> ORGANISM: Artificial Sequence

109 <220> FEATURE:

110 <223> OTHER INFORMATION: Description of Artificial Sequence: Amino acid
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 112 restricted JM22 TCR beta chain fused to c-fos
 113 leucine zipper domain.

114 <400> SEQUENCE: 4

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117	Glu	Gly	Gln	Asn	Val	Thr	Leu	Ser	Cys	Glu	Gln	Asn	Leu	Asn	His	Asp
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125	Thr	Ser	Ala	Gln	Lys	Asn	Pro	Thr	Ala	Phe	Tyr	Leu	Cys	Ala	Ser	Ser
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126																
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132																
133	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp
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134																
135	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	Pro
					165			170			175					
136																
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145 Gly Arg Ala Asp Pro Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr
 146 245 250 255
 147 Asp Gln Leu Glu Asp Lys Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn
 148 260 265 270
 149 Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala Tyr
 150 275 280 285
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 152 <211> LENGTH: 918
 153 <212> TYPE: DNA
 154 <213> ORGANISM: Artificial Sequence
 155 <220> FEATURE:
 156 <223> OTHER INFORMATION: Description of Artificial Sequence: Gene coding
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 JM22 TCR beta chain fused to c-fos leucine zipper
 domain and BirA biotinylation tag.
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 162 ccaggcgaag ggctgagatt gatctactac tcacagatag taaatgactt tcagaaaagga 180
 163 gatatacgctg aagggtacag cgtctctcggy gagaagaagg aatccttcc tctcactgtg 240
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 165 tacgagcagt acttcgggcc gggcaccagg ctcacgggtca cagaggacct gaaaaacgtt 360
 166 ttcccaccccg aggtcgctgt gtttgaacca tcagaaggac agatctccca caccggaaaag 420
 167 gccacactgg tggcctggc cacaggcttc taccggcacc acgtggagct gagctgggtgg 480
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 169 cccgcctca atgactccag atactgcctg agcagccgccc tgagggtctc gcccacccccc 600
 170 tggcagaacc cccgcacca cttccgctgt caagtcaggat tctacgggtctcggagaat 660
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 172 ggttagagcag accccggggg tctgactgat acactccaaag cggagacaga tcaacttggaa 780
 173 gacaagaagt ctgcgttgcg aaccgagatt gccaatctac taaaagagaa ggaaaaaacta 840
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 182 <223> OTHER INFORMATION: Description of Artificial Sequence: Amino acid
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 restricted JM22 TCR beta chain fused to c-fos
 leucine zipper domain and BirA biotinylation tag.
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 184
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 188 Glu Gly Gln Asn Val Thr Leu Ser Cys Glu Gln Asn Leu Asn His Asp
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 190 Ala Met Tyr Trp Tyr Arg Gln Asp Pro Gly Gln Gly Leu Arg Leu Ile
 191 35 40 45
 192 Tyr Tyr Ser Gln Ile Val Asn Asp Phe Gln Lys Gly Asp Ile Ala Glu
 193 50 55 60
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197 Thr Ser Ala Gln Lys Asn Pro Thr Ala Phe Tyr Leu Cys Ala Ser Ser
198 85 90 95
199 Ser Arg Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr
200 100 105 110
201 Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe
202 115 120 125
203 Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val
204 130 135 140
205 Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp
206 145 150 155 160
207 Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro
208 165 170 175
209 Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser
210 180 185 190
211 Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe
212 195 200 205
213 Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr
214 210 215 220
215 Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp
216 225 230 235 240
217 Gly Arg Ala Asp Pro Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr
218 245 250 255
219 Asp Gln Leu Glu Asp Lys Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn
220 260 265 270
221 Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala Tyr Gly
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224 290 295 300
225 His
226 305
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228 <211> LENGTH: 750
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: Gene coding
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234 alpha chain from clone A6 fused to c-jun leucine
235 zipper domain.
236 <400> SEQUENCE: 7
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240 aggtttacag cacagctcaa taaagccagc cagttatgtt ctctgctcat cagagactcc 240
241 cagcccagtg attcagccac ctacctctgt gccgttacaa ctgacagctg ggggaaaattg 300
242 cagtttggag cagggaccca ggttgtggtc acccccagata tccagaaccc tgaccctgcc 360
243 gtgttaccagc tgagagactc taaatccagt gacaagtctg tctgcctatt caccgatttt 420
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